


```

LOCUS       AM101885             391 bp      mRNA                      EST      18-APR-2000
DEFINITION   sd72a05.y1 Gm-cl008 glycine max cDNA GENEOME SYSTEMS CLONE ID:
              Gm-cl008-1833 5' similar to SW:TBAL_ANEPH P33623 TUBULIN ALPHA-1
CHAIN       [1] ; mRNA sequence.
ACCESSION   AM101885
VERSION     AM101885
KEYWORDS    EST.
SOURCE      AM101885.1 GI:6072498
            soybean.
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine.
REFERENCE   1 (bases 1 to 391)
AUTHORS     Shoemaker,R., Keim,P., Vodkin,L., Eipelting,J., Corvelli,V., Rhana,
              A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
              Wylie,T., Underwood,K., Stepien,M., Theising,B., Allen,M., Bowers,
              Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schuik,
              R., Ritter,E., Kohn,S., Shin,T., Jackson,I., Cardenas,M., McCann,
              R., Waterston,R. and Wilson,R.
              Public Soybean EST Project
              Unpublished (1999)
              Contact: Shoemaker R/Public Soybean EST Project
              Washington University School of Medicine
              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
              Tel: 314 286 1800
              Fax: 314 286 1810
              Email: est@watson.wustl.edu
              This clone is available through: Genome Systems, Inc. 4633 World
              Parkway Circle St. Louis, Missouri 63134 For further information
              call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314)
              Info@genomesystems.com web site: www.genomesystems.com or
              Putative full length read
              Vector to vector length is 392
              Insert length: 542 Std Error: 0.00
              Seq primer: -40RP from Glibco.
FEATURES     location/Qualifiers
             1..391
             /organism="Glycine max"
             /db_xref="taxon:3847"
             /clone="GENOME SYSTEMS CLONE ID: Gm-cl008-1833"
             /clone_lib="Gm-cl008"
             /lab_host="DH10B"
             /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; This
             cDNA library was constructed from mRNA isolated from whole
             young pods, approximately 2cm long, of 12-week-old
             greenhouse grown plants. The library was prepared using
             the Life Technologies superscript cDNA library
             construction kit. Complementary DNA was synthesized from
             mRNA using a poly (dT) sequence with a NotI restriction
             site. SalI linkers adapters were ligated to the
             blunt-ended cDNA fragments followed by NotI digestion. The
             cDNA fragments were directionally cloned into the
             NotI-SalI restriction site of the pSPORT1 vector. The
             ligated cDNA fragments were transformed into E. coli
             Electromax DH10B host cells. This library was constructed
             by Dr. Lila Vodkin and Dr. Anu Khanna."
BASE COUNT   87 a 69 c 108 g 127 t
ORIGIN
alignment_scores:
  Quality: 7.00 Length: 7
  Ratio: 1.000 Gaps: 0
  Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
  US-09-126-945B-2_COPY_236_243 x AM101885/rev
Align seg 1/1 to reverse of: AM101885 from: 1 to: 391
2 AspSergIuValasPserSer 8
seq_name: gb_est80:BE841998

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|||||
234 GATTCTGGAAGTGAATTCAGT 214
seq_name: gb_est80:BE841998
seq_documentation_block:
LOCUS       BE841998             408 bp      mRNA                      EST      22-SEP-2000
DEFINITION   MR4-ST0098-280600-010-c07 ST0098 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BE841998
VERSION     BE841998.1 GI:10274376
KEYWORDS    EST.
SOURCE      human.
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 408)
AUTHORS     Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Britones,M.R.,
              Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
              Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
              Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,
              M.J., Soares,F., Brentani,I.R.R., Reis,L.F., de Souza,S.J. and
              Simpson,A.J.
              Shotgun sequencing of the human transcriptome with ORF expressed
              sequence tags
              Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
              20202663
              Contact: Simpson A.J.G.
              Laboratory of Cancer Genetics
              Ludwig Institute for Cancer Research
              Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
              Brazil
              Tel: +55-11-2704922
              Fax: +55-11-2707001
              Email: asimpson@ludwig.org.br
              This sequence was derived from the FAPESP/LICR Human Cancer Genome
              Project. This entry can be seen in the following URL
              (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-MR4-ST0098-280
              600-010-c07&ts3=2000-06-28&ts4=1)
              Seq primer: puc 18 forward
              High quality sequence start: 37
              High quality sequence stop: 408.
FEATURES     location/Qualifiers
             1..408
             /organism="Homo sapiens"
             /db_xref="taxon:9606"
             /clone_lib="ST0098"
             /dev_stage="Adult"
             /note="Organ: stomach; Vector: puc18; Site_1: SmaI;
             Site_2: SmaI; A mini-library was made by cloning products
             derived from ORESTES PCR (U.S. Letters Patent application
             No. 196,716 - Ludwig Institute for Cancer Research)
             profiles into the puc 18 vector. Reverse transcription of
             tissue mRNA and cDNA amplification were performed under
             low stringency conditions."
BASE COUNT   159 a 66 c 76 g 107 t
ORIGIN
alignment_scores:
  Quality: 7.00 Length: 7
  Ratio: 1.000 Gaps: 0
  Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
  US-09-126-945B-2_COPY_236_243 x BE841998/rev
Align seg 1/1 to reverse of: BE841998 from: 1 to: 408
2 AspSergIuValasPserSer 8
|||||
308 GATTCTGGAAGTGAATTCAGTCC 288
seq_name: gb_est97:BG159086

```

seq_documentation_block: 549 bp mRNA EST 06-FEB-2001
 LOCUS BC159088 RH122_17_F11_b1_A003 Rhizome2 (RH122) Sorghum proplinqum cDNA, mRNA
 DEFINITION
 ACCESSION BG159088
 VERSION BG159088.1 GI:12692752
 KEYWORDS EST
 SOURCE Sorghum proplinqum.
 ORGANISM Sorghum proplinqum.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoidae; Andropogonae; Sorghum.
 1 (bases 1 to 549)
 Cordonnier-Pratt,M.-M., Gingle,A., Paterson,A., Sudman,M. and Pratt
 L.H.
 TITLE An EST database from Sorghum: Sorghum proplinqum rhizomes
 JOURNAL Unpublished (2000)
 COMMENT Contact: Cordonnier-Pratt MM
 Department of Botany
 The University of Georgia
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 542 1805
 Email: mmp@prattuga.edu
 Seq primer: JEN REV
 High quality sequence stop: 486
 POLYA-NO.

FEATURES
 source
 1. 549
 /location/Qualifiers
 /organism="Sorghum proplinqum"
 /db_xref="taxon:132711"
 /clone_1lb="Rhizome2 (RH122)"
 /note="Organ: Rhizomes; Vector: pBluescript II from Lambda
 Zap II; Site_1: XhoI; Site_2: EcoRI; The library was made
 from poly-A RNA in the cloning vector Lambda Zap II.
 Clones to be sequenced were prepared by mass excision."
 133 a 133 c 156 g 130 t

BASE COUNT 130 a 133 c 156 g 130 t
 ORIGIN

alignment_scores:
 Quality: 7.00 Length: 7
 Ratio: 1.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-126-945B-2_COPY_236_243 x BG159088 ..
 Align seg 1/1 to: BG159088 from: 1 to: 549

1 ThrAspSerGluValAspSer 7
 |||||||
 523 ACTGACACTGAAGTTCCTCC 543

seq_name: gb_cst16:AI119983

seq_documentation_block: 555 bp mRNA EST 02-SEP-1998
 LOCUS AI119983 uc25601.r1 Soares_mammary_gland_NbMWG Mus musculus cDNA clone
 DEFINITION IMAGE:1398984 5' similar to gb:J04982.cds1 ADP ATP CARRIER PROTEIN,
 HEART/SKELETAL MUSCLE ISOFORM (HUMAN): gb:U27315 Mus musculus
 adenine nucleotide translocase-1 (MUSE);, mRNA sequence.
 AI119983
 VERSION AI119983.1 GI:3520307
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 555)
 Morita,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

TITLE Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 JOURNAL Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 COMMENT The WashU-HMI Mouse EST Project
 Unpublished (1996)
 Contact: Maria M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LML; contact the
 IMAGE Consortium (info@image.lml.gov) for further information.
 MGI:910700
 Seq primer: -28n13 rev2 ET from Amersham
 High quality sequence stop: 258.

FEATURES
 source
 1. 555
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:1398984"
 /clone_1lb="Soares_mammary_gland_NbMWG"
 /sex="male"
 /tissue="mammary gland"
 /dev_stage="4 weeks"
 /lab_host="DH10B"
 /note="Organ: mammary gland; Vector: pRT73D-Pac (Pharmacia
) with a modified polylinker; Site_1: Not I; Site_2: Eco
 RI; 1st strand cDNA was primed with a Not I - oligo(dT)
 primer (5'
 TGTTCACATCTGACAGTGCAGCGCCGCAATGCTTTTGTGTGTGTGTGTGTGTGT
 T 3'); double-stranded cDNA was ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of the modified pRT73 vector.
 RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
 constructed and normalized by Benito Soares and M. Fatima
 Bonaldo."

BASE COUNT 155 a 101 c 151 g 147 t 1 others
 ORIGIN

alignment_scores:
 Quality: 7.00 Length: 7
 Ratio: 1.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-126-945B-2_COPY_236_243 x AI119983/rev ..
 Align seg 1/1 to reverse of: AI119983 from: 1 to: 555

2 AspSerGluValAspSer 8
 |||||||
 50 GACTCCGAAGTACACACTCT 30

seq_name: gb_gss12:A0510431

seq_documentation_block: 563 bp DNA GSS 04-MAY-1999
 LOCUS A0510431 ndxb0095b16f CGCI Rice BAC Library Oryza sativa genomic clone
 DEFINITION ndxb0095b16f, DNA sequence.
 A0510431
 ACCESSION A0510431 GI:4733035
 VERSION A0510431.1
 KEYWORDS GSS.
 SOURCE Oryza sativa.
 ORGANISM Oryza sativa.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzoae; Oryza.
 1 (bases 1 to 563)
 Wing,R.A. and Dean,R.A.

TITLE A BAC End Sequencing Framework to Sequence the Rice Genome
JOURNAL Unpublished (1998)
COMMENT Contact: Ming RA
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: GGAAACAGCTGACATC
Class: BAC ends
High quality sequence stop: 411.
Location/Qualifiers
1. 563
/organism="Oryza sativa"
/strain="Japonica"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
/clone="ndxb0095M16r"
/clone_lib="CUGI Rice BAC Library"
/tissue_type="leaf"
/lab_host="E. coli DH10B"
/note="Vector: pBelobact1. Site_1: HindIII. Site_2: HindIII. Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."

BASE COUNT 179 a 97 c 90 g 197 t
ORIGIN

alignment_scores:
Quality: 7.00 Length: 7
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

Alignment block:
US-09-126-945B-2_COPY_236_243 x AQ510431 ..
Align seg 1/1 to: AQ510431 from: 1 to: 563

2 AspSerGluValAspSerSer 8
|||||
137 GATCGGAAGTGTGACTCATCC 157

seq_name: gb_est27:AJ393331

seq_documentation_block:
LOCUS AJ393331 803 bp mRNA EST 25-JAN-2001
DEFINITION AJ393331 dkfz426 Gallus gallus cDNA clone 15c3r1, mRNA sequence.
ACCESSION AJ393331
VERSION AJ393331.1 GI:7122087
KEYWORDS EST.
SOURCE chicken.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 803)

AUTHORS Abdurakhmanov, I., Lodygin, D., Gerolt, P., Arakawa, H., Law, A., Plachy, J., Korn, B. and Buerstedde, J.M.
TITLE A large database of chicken bursal ESTs as a resource for the analysis of vertebrate gene function
JOURNAL Genome Res. 10 (12), 2062-2069 (2000)
MEDLINE 20568495
COMMENT Contact: Buerstedde JM
Cellular Immunology
Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: <http://genetics.hpi.uni-hamburg.de/dt40est.html>.

FEATURES
source
1. 803
/organism="Gallus gallus"
/strain="CB"
/db_xref="taxon:9031"
/clone="15c3r1"
/clone_lib="dkfz426"
/tissue_type="Bursa of Fabricius"
BASE COUNT 265 a 155 c 186 g 194 t 3 others
ORIGIN

alignment_scores:
Quality: 7.00 Length: 7
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

Alignment block:
US-09-126-945B-2_COPY_236_243 x AJ393331/rev ..
Align seg 1/1 to reverse of: AJ393331 from: 1 to: 803

1 ThrAspSerGluValAspSer 7
|||||
587 ACAGATCTGTGAGTGTGACTCC 567

seq_name: gb_est92:BF795883

seq_documentation_block:
LOCUS BF795883 917 bp mRNA EST 12-JAN-2001
DEFINITION 602259125F1 NIH-MGC-85 Homo sapiens cDNA clone IMAGE:4342183 5', mRNA sequence.
ACCESSION BF795883
VERSION BF795883.1 GI:12100937
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 917)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@email.nih.gov
Tissue Procurement: Louis Staudt, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
<http://image.llnl.gov>
Plate: LHAM9957 row: b column: 08
High quality sequence stop: 633.
Location/Qualifiers
1. 917
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4342183"
/clone_lib="NIH-MGC-85"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"

/note="Organ: lymph; Vector: PCMV-SpOrf6; Site:1: NotI;
Site:2: SalI; Cloned unidirectionally; oligo-dt primed.
Average insert size 1.867 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH-MGC Library."

BASE COUNT 215 a 229 c 281 g 191 t 1 others
ORIGIN

alignment_scores:
Quality: 7.00 Length: 7
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

us-09-126-945b-2_COPY_236_243 x BF795883 ..

Align seg 1/1 to: BF795883 from: 1 to: 917

2 AappSergIuValaapSergSer 8
|||||
711 GACTCGGAAGTTCCTCTCT 731

seq_name: gb_est81:BE978811

seq_documentation_block:

LOCUS BE978811 77 bp mRNA EST 04-OCT-2000
DEFINITION b883b08.y1 Drosophila melanogaster adult testis library drosophila
melanogaster cDNA b883b08 5', mRNA sequence.
ACCESSION BE978811
VERSION BE978811.1 GI:10610669
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscophora; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 77)
AUTHORS Andrews, J., Bouffard, G. and Oliver, B.

TITLE Drosophila melanogaster testis expressed sequence tags
JOURNAL Unpublished (1999)
COMMENT Contact: Brian Oliver
Laboratory of Cellular and Developmental Biology
NIDDK, National Institutes of Health
6 Center Drive MSC 2715, Bldg 6, Rm B1-13, Bethesda, MD 20892 USA
Fax: (301) 496 5239
Email: Oliver@helix.nih.gov,
http://www.nidk.nih.gov/intram/people/dolliver.htm
tissue isolation and library construction performed at the National
Institute of Diabetes and Digestive and Kidney Diseases, NIH (see
http://www.nidk.nih.gov/intram/people/dolliver.htm). DNA sequencing
and analyses performed by National Institutes of Health Intramural
Sequencing Center (NISC; see http://www.nisc.nih.gov).

Plate: 83 row: b column: 08
Seq primer: M13RP1 reverse primer (ABT).
Location/Qualifiers

FEATURES

source

1..77
/organism="Drosophila melanogaster"
/strain="y1" w[67c1]/y"
/db_xref="taxon:7227"
/clone="b883b08"
/clone_lib="Drosophila melanogaster adult testis library"
/sex="male"
/dev_stage="1-5 day adult"
/lab_host="SOLR (Stratagene)"
/note="Organ: testis; Vector: pBluescript SK (Stratagene);
Site:1: EcoR I; Site:2: Xho I; Testes dissected from 1-5
day adult y1" w[67c1]/y males raised at 25°C. RNA
isolated using Trizol (Life Technologies) and a single
round of Poly(A)+ selection using Oligotex (Qiagen). cDNA
library constructed using Stratagene ZAP-cDNA synthesis
kit. Oligo dt-primed, size fractionated -1-6 kb, and
directionally cloned at EcoRI and XhoI in Uni-ZAP XR.

Following a single round of amplification pBluescript SK
phagemids were mass excised. A distribution channel for
clones is being sought, but not currently available.
Requests for clones cannot be honored."

BASE COUNT 19 a 22 c 15 g 21 t
ORIGIN

alignment_scores:
Quality: 6.00 Length: 6
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

us-09-126-945b-2_COPY_236_243 x BE978811/rev ..

Align seg 1/1 to reverse of: BE978811 from: 1 to: 77

3 SergIuValaapSergSer 8
|||||
45 TCGGAAGTTCGATTCAGT 28

seq_name: gb_est111:231199

seq_documentation_block:

LOCUS 231199 143 bp mRNA EST 24-JAN-1995
DEFINITION M875592 Mouse testis T-ZAP Mus musculus cDNA, mRNA sequence.
ACCESSION 231199
VERSION 231199.1 GI:633431
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 143)
AUTHORS Yuan, L., Liu, J.G. and Hoog, C.

TITLE Rapid cDNA sequencing in combination with RNA expression studies
identifies a large number of male germ cell-specific sequence tags
JOURNAL Biol. Reprod. 52, 131-138 (1995)
MEDLINE 95226560
COMMENT Contact: C. Hoog
Dept. of Molecular Genetics
Karolinska Institutet
Box 60400, 1401 Stockholm, SWEDEN.
Location/Qualifiers

FEATURES

source

1..143
/organism="Mus musculus"
/strain="CBA"
/db_xref="taxon:10090"
/clone_lib="House testis T-ZAP"
/note="Testis from adult mouse"
BASE COUNT 33 a 39 c 29 g 41 t 1 others
ORIGIN

alignment_scores:
Quality: 6.00 Length: 6
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

us-09-126-945b-2_COPY_236_243 x 231199 ..

Align seg 1/1 to: 231199 from: 1 to: 143

3 SergIuValaapSergSer 8
|||||
58 AGCGAAGTTCGATTCCTCC 75

seq_name: gb_est81:BE938486

seq_documentation_block:

LOCUS BE938486 163 bp mRNA EST 02-OCT-2000

```

DEFINITION RC0-TN0079-290800-023-b06 TN0079 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE938486
VERSION BE938486.1 GI:10465862
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 163)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., de Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=6t2-RC0-TN0079-290
800-023-b06&cl=2000-08-29&cl=1)
Seq primer: puc 18 forward
High quality sequence start: 43
High quality sequence stop: 163.
Location/Qualifiers
source 1..163
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="TN0079"
/dev_stage="Adult"
/note="Organ: testis, normal; Vector: puc18; Site: 1; Smal;
Site: 2; Smal; A mini-library was made by cloning products
derived from ORESMES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 38 a 43 c 43 g 39 t
ORIGIN
alignment_scores:
Quality: 6.00 Length: 6
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
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Align seg 1/1 to: BE938486 from: 1 to: 163
3 SerGIuValAspSerSer 8
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19 TCAGAGCTAGACACACG 36
seq_name: gb_gss35:B42379
seq_documentation_block:
LOCUS B42379 167 bp DNA GSS 18-OCT-1997
DEFINITION HS-1055-B2-C09-MF-ab1 CIT Human Genomic Sperm Library C Homo
sapiens genomic clone Plate-CT 777 Col-18 Row-F, DNA sequence.
ACCESSION B42379
VERSION B42379.1 GI:2546631

```

```

KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 167)
Mahairas, G.G., Zackrone, K.D., Smith, T., Tipton, S., Schmidt, S.,
Traicoff, R., Abajian, C., Blanchard, A., West, A. and Hood, L.E.
Construction of a Characterized Clone Resource for Genomic
Sequencing: Generation and Preliminary Analysis of 20,000 Sequence
Tagged Connectors
Unpublished (1997)
CONTACT: Mahairas GG, Zackrone KD, Hood L
University of Washington
Seattle, WA 98195, USA
Tel: (206) 616-8744
Fax: (206) 685-7301
Email: kzackrone@u.washington.edu
Sequence Tagged Connector
Plate: CT 777 row: F column: 18
Class: BAC ends
High quality sequence stop: 167.
Location/Qualifiers
source 1..167
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Plate-CT 777 Col-18 Row-F"
/sex="M"
/note="Organ: sperm; Vector: pBelBAC11; BAC Clones in
E-Coll DH10B"
BASE COUNT 43 a 40 c 40 g 43 t 1 others
ORIGIN
alignment_scores:
Quality: 6.00 Length: 6
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-126-945B-2_COPY_236_243 x B42379/rev ..
Align seg 1/1 to reverse of: B42379 from: 1 to: 167
3 SerGIuValAspSerSer 8
|||||
96 TCAGAACTGATTCACGT 79
seq_name: gb_est54:BB019091
seq_documentation_block:
LOCUS BB019091 178 bp mRNA EST 22-JUN-2000
DEFINITION BB019091 RIKEN full-length enriched, adult male testis (DH10B) Mus
musculus cDNA clone 4930583H10 3', mRNA sequence.
ACCESSION BB019091
VERSION BB019091.1 GI:8190850
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 178)
Kono, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci
P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.,
Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata
Y., Shigemoto, Y., Shinagawa, A., Shitaki, T., Sogabe, Y., Sugihara, Y.,
Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomioka, N., Toya
T., Tsunoda, Y., Watanabe, S., Watanabe, S., Yamamura, T., Yamataka, I.

```

TITLE
JOURNAL
COMMENT
, Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
Riken Mouse ESTs (Konno, H., et al.)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center,
Genome Science Laboratory
The Institute of Physical and Chemical Research (RIKEN), Genomic
Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
Email: genome-res@r.riken.go.jp,
URL: http://genome.rtc.riken.go.jp/
Carinci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagao, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermolabile and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kikunishi, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carinci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carinci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.

FEATURES

source

Location/Qualifiers

1. 178
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="493058310"
/clone_1lb="RIKEN full-length enriched, adult male testis (DH10B)"
/sex="male"
/tissue="testis"
/dev_stage="adult"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5']
GAGAGAGAGATCCAGAGCTTTTCTTTTCTTTT 3', cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5']
GAGAGAGATCTCGAGTTAATTAATTAATCCCCCCCCC 3'. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified plasmid vector KS(+) after bulk excision from Lambda phage I. Cloning sites, 5' end: SalI; 3' end: BamHI."

BASE COUNT

54 a 32 c 33 g 33 t

Alignment_scores:

Quality: 6.00 Length: 6
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

Alignment_block:

US-09-126-945B-2_COPY_236_243 x BB019091 ..

Align seg 1/1 to: BB019091 from: 1 to: 178

3 SarguValaPserSer 8

|||||

40 AGCAGATGACACAGCAGT 57

seq_name: gb-gss18:A0925777

seq_documentation_block:

LOCUS A0925777 183 bp DNA GSS 21-DEC-1999
DEFINITION RPI-23-297P13 TV RPI-23 Mus musculus genomic clone RPI-23-297P13
DNA sequence.

ACCESSION A0925777

VERSION A0925777.1 GI:6614697

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 183)
Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akhmet, B., Levins, M., McGann, S., Teagay, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPI-23

REFERENCE

AUTHORS

JOURNAL

COMMENT

TITLE

UNPUBLISHED (1999)

CONTACT: Shaying Zhao

DEPARTMENT: Eukaryotic Genomics

THE INSTITUTE FOR GENOMIC RESEARCH

9712 Medical Center Dr., Rockville, MD 20850, USA

TEL: 301 838 0208

FAX: 301 838 0208

EMAIL: szhao@ligr.org

CLONES ARE DERIVED FROM THE MOUSE BAC LIBRARY RPI-23. FOR BAC

LIBRARY AVAILABILITY, PLEASE CONTACT PIETER DE JONG

(pieter@ligr.med.buffalo.edu). CLONES MAY BE PURCHASED FROM

BACPAC RESOURCES (http://bacpac.med.buffalo.edu/orderingframe.htm)

OR FROM RESEA CH GENETICS (info@resgen.com). BAC END PAGE:

http://www.ligr.org/tid/bac_ends/mouse/bac_end_intro.html

PLATE: 297 ROW: P COLUMN: 13

SEG PRIMER: T7

CLASS: BAC ends.

FEATURES

source

Location/Qualifiers

1. 183
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPI-23-297P13"
/clone_1lb="RPI-23"
/sex="Female"
/lab_host="DH10B"
/note="Organ: Kidney/Brain; Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRV methylase. Size selected DNA was cloned into the pBAC3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."

BASE COUNT

66 a 39 c 32 g 46 t

Alignment_scores:

Quality: 6.00 Length: 6
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

Alignment_block:

US-09-126-945B-2_COPY_236_243 x A0925777 ..

Align seg 1/1 to: A0925777 from: 1 to: 183

3 SarguValaPserSer 8

|||||

seq_name: gb-est32:AV057324

seq_documentation_block:

LOCUS AV057324 187 bp mRNA EST 23-JUN-1999
 DEFINITION AV057324 Mus musculus pancreas C57BL/6J adult Mus musculus cDNA
 clone 1810045G16, mRNA sequence.

ACCESSION AV057324
 VERSION AV057324.1 GI:5157071

KEYWORDS

EST.

SOURCE

house mouse.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 187)

AUTHORS

Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara
 A., Hayatsu, N., Horii, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J.,
 Kikuchi, N., Kojima, Y., Matsuyama, T., Nitsuma, H., Oda, H., Owa, C.,
 Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara
 Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tomlinaga, N.,
 Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M.,
 Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.

TITLE

RIKEN Mouse ESTs

JOURNAL

Unpublished (1999)

COMMENT

Contact: Chie Owa

Genome

Genome Science Laboratory

RIKEN

3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan

Tel:

81-298-36-9145

Fax:

81-298-36-9098

Email: genome-res@rtc.riken.go.jp

Thermolabile and thermocyclization of thermolabile enzymes by
 trehalose and its application for the synthesis of full length cDNA
 (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))

Transcriptional sequencing: A method for DNA sequencing using RNA
 polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))

Please visit our web site (<http://genome.rtc.riken.go.jp>) for
 further details.

FEATURES

Location/Qualifiers

source

1..187

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="1810045G16"

/clone_lib="Mus musculus pancreas C57BL/6J adult"

/sex="male"

/tissue_type="pancreas"

/dev_stage="adult"

BASE COUNT

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ORIGIN

alignment_scores:

Quality: 6.00 Length: 6
 Ratio: 1.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-126-945b-2_COPY_236_243 x AV057324 ..

Align seg 1/1 to: AV057324 from: 1 to: 187

3 SerGIuValaspSerSer 8

|||||

1 TCAGAGCTCGATTCTACT 18